

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/096,500

OIPE

#8

DATE: 06/22/98
TIME: 11:01:53

INPUT SET: S26845.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Ashkenazi, Avi J.
Baker, Kevin
Chuntharapai, Anan
Gurney, Austin
Kim, Kyung Jin
Wood, William

ENTERED

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 12-Jun-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911
(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5416
(B) TELEFAX: 650/952-9881

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47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 259 amino acids

51 (B) TYPE: Amino Acid

52 (D) TOPOLOGY: Linear

53

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

56 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
57 1 5 10 15

58

59 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
60 20 25 30

61

62 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
63 35 40 45

64

65 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
66 50 55 60

67

68 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
69 65 70 75

70

71 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
72 80 85 90

73

74 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
75 95 100 105

76

77 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
78 110 115 120

79

80 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
81 125 130 135

82

83 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
84 140 145 150

85

86 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
87 155 160 165

88

89 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
90 170 175 180

91

92 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
93 185 190 195

94

95 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
96 200 205 210

97

98 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
99 215 220 225

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100
101 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
102 230 235 240
103
104 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
105 245 250 255
106
107 Ile Val Phe Val
108 259
109

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

112 (A) LENGTH: 1180 base pairs
113 (B) TYPE: Nucleic Acid
114 (C) STRANDEDNESS: Single
115 (D) TOPOLOGY: Linear
116
117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

118
119
120
121 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50
122
123 ATTTTGGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100
124
125 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150
126
127 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195
128 Met
129 1
130
131 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234
132 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
133 5 10
134
135 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273
136 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
137 15 20 25
138
139 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312
140 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
141 30 35 40
142
143 CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351
144 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
145 45 50
146
147 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
148 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
149 55 60 65
150
151 AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
152 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser

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153		70		75	
154					
155	AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA	468			
156	Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys				
157	80 85 90				
158					
159	TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA	507			
160	Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg				
161	95 100 105				
162					
163	GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT	546			
164	Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn				
165	110 115				
166					
167	GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC	585			
168	Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys				
169	120 125 130				
170					
171	CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG	624			
172	Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp				
173	135 140				
174					
175	GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC	663			
176	Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala				
177	145 150 155				
178					
179	ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC	702			
180	Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr				
181	160 165 170				
182					
183	AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG	741			
184	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met				
185	175 180				
186					
187	AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG	780			
188	Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu				
189	185 190 195				
190					
191	ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT	819			
192	Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala				
193	200 205				
194					
195	GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA	858			
196	Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro				
197	210 215 220				
198					
199	GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT	897			
200	Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro				
201	225 230 235				
202					
203	GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC	936			
204	Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile				
205	240 245				

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206
207   ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970
208   Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
209       250               255               259
210
211   GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020
212
213   AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070
214
215   TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120
216
217   AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170
218
219   AAAAAAAAAA 1180
220
221 (2) INFORMATION FOR SEQ ID NO:3:
222
223     (i) SEQUENCE CHARACTERISTICS:
224         (A) LENGTH: 299 amino acids
225         (B) TYPE: Amino Acid
226         (D) TOPOLOGY: Linear
227
228     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
229
230   Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
231   -40               -35               -30
232
233   Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
234   -25               -20               -15
235
236   Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
237   -10               -5               1               5
238
239   Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
240               10               15               20
241
242   Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
243               25               30               35
244
245   Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
246               40               45               50
247
248   Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
249               55               60               65
250
251   Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
252               70               75               80
253
254   Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
255               85               90               95
256
257   Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
258               100              105              110

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SEQUENCE VERIFICATION REPORT
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Original Text